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OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 19:29:08 ; Search time 76 Seconds  
(without alignments)  
645.899 Million cell updates/sec

Title: SEQ1-191TO220

Perfect score: 30

Sequence: 1 taatatgctctgtatcatgctatgct 30

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapect 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29.6	98.7	30324	US-09-949-016-16037	Sequence 16037, A
2	21.8	72.7	601	US-09-949-016-52103	Sequence 52103, A
3	21.8	72.7	264206	US-09-949-016-12731	Sequence 12731, A
4	21.8	72.7	264304	US-09-949-016-13249	Sequence 13249, A
5	21.2	70.7	2982	US-09-710-279-3385	Sequence 3385, Ap
6	21.2	70.7	3226	US-09-710-279-4024	Sequence 4024, Ap
7	20.8	69.3	138282	US-09-949-016-15307	Sequence 15307, A
8	20.2	67.3	35574	US-09-949-016-45077	Sequence 45077, A
9	20.2	67.3	35574	US-09-949-016-14511	Sequence 14511, A
10	20.2	67.3	165651	US-09-949-016-13032	Sequence 13032, A
11	20.2	67.3	253375	US-09-949-016-12849	Sequence 12849, A
12	20.2	67.3	253375	US-09-949-016-12849	Sequence 12849, A
13	20.2	67.3	253375	US-09-949-016-12849	Sequence 12849, A
14	19.8	66.0	457	US-09-949-016-185760	Sequence 185760, A
15	19.8	66.0	1473	US-09-244-805-42	Sequence 42, Appl
16	19.6	65.3	311	US-09-513-999C-12912	Sequence 12912, A
17	19.6	65.3	373	US-09-513-999C-12913	Sequence 12913, A
18	19.6	65.3	501	US-09-513-999C-3844	Sequence 3844, Ap
19	19.6	65.3	601	US-09-949-016-132114	Sequence 13211, A
20	19.6	65.3	43192	US-09-949-016-15466	Sequence 15466, A
21	19.6	65.3	103712	US-09-949-016-13058	Sequence 13058, A
22	19.2	64.0	601	US-09-949-016-132115	Sequence 132115, A
23	19.2	64.0	1764	US-09-620-312D-548	Sequence 548, App
24	19.2	64.0	49487	US-09-949-016-15721	Sequence 15721, A
25	19	63.3	624	US-09-270-767-4747	Sequence 4747, Ap
26	19	63.3	624	US-09-270-767-40029	Sequence 20029, A
27	19	63.3	3001	US-09-539-333D-199	Sequence 199, App

28	19	63.3	3735	4	US-09-543-681A-2102	Sequence 2102, Ap
29	19	63.3	5488	4	US-09-949-016-17039	Sequence 17039, A
30	19	63.3	154626	4	US-09-949-016-14000	Sequence 14000, A
31	19	63.3	161124	4	US-09-949-016-11760	Sequence 11760, A
32	19	63.3	294836	4	US-09-949-016-15974	Sequence 15974, A
33	18.8	62.7	601	4	US-09-949-016-132112	Sequence 132112, A
34	18.8	62.7	13401	4	US-09-949-016-12239	Sequence 12239, A
35	18.8	62.7	13402	4	US-09-949-016-14595	Sequence 14595, A
36	18.8	62.7	43132	4	US-09-949-016-15466	Sequence 15466, A
37	18.6	62.0	4372	4	US-09-949-016-185761	Sequence 185761, A
38	18.6	62.0	479	4	US-09-949-016-185757	Sequence 185757, A
39	18.6	62.0	601	4	US-09-949-016-88182	Sequence 88182, A
40	18.6	62.0	601	4	US-09-949-016-88845	Sequence 88845, A
41	18.6	62.0	601	4	US-09-949-016-154502	Sequence 154502, A
42	18.6	62.0	601	4	US-09-949-016-162928	Sequence 162928, A
43	18.6	62.0	601	4	US-09-949-016-195810	Sequence 195810, A
44	18.6	62.0	5900	4	US-09-949-016-14621	Sequence 14621, A
45	18.6	62.0	5993	3	US-09-383-630-1	Sequence 1, Appl1

#### ALIGNMENTS

```
RESULT 1
US-09-949-016-16037
Sequence 16037, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16037
LENGTH: 30324
TYPE: DNA
ORGANISM: Human
US-09-949-016-16037

Query Match          98.7%; Score 29.6; DB 4; Length 30324;
Best Local Similarity 96.7%; Pred. No. 0.0094;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTATATGCTATATGCT 30
Db      25379 TAAATATGCTCTGTATATGCTATATGCT 25408

RESULT 2
US-09-949-016-52103/C
Sequence 52103, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 52103  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-52103

Query Match  
Best Local Similarity 72.7%; Score 21.8; DB 4; Length 601;  
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATATGCTATAT 27  
DB 87 TATATATGCGCTATATATATATGCTATAT 61

RESULT 3  
US-09-949-016-12731  
; Sequence 12731, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12731  
; LENGTH: 264206  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12731

Query Match  
Best Local Similarity 72.7%; Score 21.8; DB 4; Length 264206;  
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATATGCTATAT 27  
DB 135523 TATATATGCGCTATATATATGCTATAT 135549

RESULT 4  
US-09-949-016-13249  
; Sequence 13249, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13249  
; LENGTH: 264304

;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-13249

Query Match  
Best Local Similarity 72.7%; Score 21.8; DB 4; Length 264304;  
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATATGCTATAT 27  
DB 135523 TATATATGCGCTATATATATGCTATAT 135549

RESULT 5  
US-09-710-279-3385  
; Sequence 3385, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3385  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-3385

Query Match  
Best Local Similarity 70.7%; Score 21.2; DB 4; Length 2982;  
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATATGCTCTGTTATATATGCTATATGCT 30  
DB 42 AATGACTCTGTAATATATGCTTATGCT 69

RESULT 6  
US-09-710-279-4024  
; Sequence 4024, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4024  
; LENGTH: 3226  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-4024

Query Match  
Best Local Similarity 70.7%; Score 21.2; DB 4; Length 3226;  
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATATGCTCTGTTATATATGCTATATGCT 30

Db 3154 AATGACTCTGTATATATGCTTATGCT 3181

RESULT 7  
US-09-949-016-15307/c  
; Sequence 15307, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ. ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15307  
; LENGTH: 138282  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15307

Query Match 69.3%; Score 20.8; DB 4; Length 138282;  
Best Local Similarity 84.6%; Pred. No. 48;  
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATATGCTCTGTATATGCTATAT 27  
Db 25404 ATATATGCTATATATATATGCTATAT 25379

RESULT 8  
US-09-949-016-45077  
; Sequence 45077, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ. ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45077  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-45077

Query Match 67.3%; Score 20.2; DB 4; Length 601;  
Best Local Similarity 81.5%; Pred. No. 35;  
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27  
Db 525 TTAATGCTCTCTTGTATATGCTATAT 551

RESULT 9

US-09-949-016-11843/c  
; Sequence 11843, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ. ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11843  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11843

Query Match 67.3%; Score 20.2; DB 4; Length 35574;  
Best Local Similarity 81.5%; Pred. No. 67;  
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27  
Db 164 TATATATGCTATATATATATGCTATAT 138

RESULT 10  
US-09-949-016-14511/c  
; Sequence 14511, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ. ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14511  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14511

Query Match 67.3%; Score 20.2; DB 4; Length 35574;  
Best Local Similarity 81.5%; Pred. No. 67;  
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27  
Db 164 TATATATGCTATATATATATGCTATAT 138

RESULT 11  
US-09-949-016-13032  
; Sequence 13032, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13032
; LENGTH: 165651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(165651)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13032
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Query Match      67.3%; Score 20.2; DB 4; Length 165651;
Best Local Similarity 81.5%; Pred. No. 86;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
Db      67257 TTAATGCTCTTGTGTAATATGCTATAT 67283
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RESULT 12
US-09-949-016-12849
; Sequence 12849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12849
; LENGTH: 253375
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(253375)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12849
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Query Match      67.3%; Score 20.2; DB 4; Length 253375;
Best Local Similarity 81.5%; Pred. No. 92;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
Db      5116 TATATATACTATGTATATATATATATAT 5142
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RESULT 13
US-09-949-016-12849/c
; Sequence 12849, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12849
; LENGTH: 253375
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(253375)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12849
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Query Match      67.3%; Score 20.2; DB 4; Length 253375;
Best Local Similarity 81.5%; Pred. No. 92;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
Db      5457 TATATATACTATGTATATATATATATAT 5431
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RESULT 14
US-09-949-016-185760/c
; Sequence 185760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185760
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-185760
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Query Match      66.0%; Score 19.8; DB 4; Length 457;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
Db      308 TATATATATATGTATATATATATATATAT 282
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RESULT 15
US-09-244-805-42/c
; Sequence 42, Application US/09244805
; Patent No. 6699660
```

GENERAL INFORMATION:  
; APPLICANT: Worley, Paul F.  
; APPLICANT: Lanahan, Anthony  
; APPLICANT: Goetz, Bernard  
; APPLICANT: Heimlich, Holger  
; APPLICANT: Kuner, Rohini  
; APPLICANT: Scheek, Sigrid  
; APPLICANT: Nikolich, Karoly  
; APPLICANT: Zhukovski, Eugene  
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 10496/004001  
; CURRENT APPLICATION NUMBER: US/09/244,805  
; CURRENT FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/074,518  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: 60/074,135  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 1473  
; TYPE: DNA  
; ORGANISM: Eukaryote  
US-09-244-805-42

Query Match 66.0%; Score 19.8; DB 4; Length 1473;  
Best Local Similarity 84.0%; Pred. No. 59;  
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATGCTCTGTATATGCTATATGCT 30  
||| ||| : ||| ||| ||| |||  
Db 647 ATGCTTGAATATCTGCTATATGCT 623

Search completed: February 14, 2005, 22:35:59  
Job time : 80 secs

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OM nucleic - nucleic search, using bw model

Run on: February 14, 2005, 21:06:43 ; Search time 427 Seconds  
(without alignments)  
415.907 Million cell updates/sec

Title: SEQ1-191T0220  
Perfect score: 30  
Sequence: 1 taatatgctctgcttatcgtcatatgct 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: N\_Geneseq\_16Dec04:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001s:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	21.2	70.7	1273	ADCB7532
2	21.2	70.7	2982	AAH54021
3	21.2	70.7	3225	AAH54650
4	20.8	69.3	1781	ADRB7041
5	20.6	68.7	6291	ABL06646
6	20.6	68.7	3221	ABAI6118
7	20.6	68.7	39198	AAFS8067
8	20.6	68.7	46553	AAK81745
9	20.6	68.7	46553	AAK67926
10	20.6	68.7	59001	ADH54712
11	20.6	68.7	167932	ADL13501
12	20.4	68.0	4141	ABL05214
13	20.4	68.0	4164	ABL05338
14	20.2	67.3	2967	ABT18070
15	20.2	67.3	3423	ABT19884
16	20.2	67.3	15548	ABL34155
17	20.2	67.3	50000	ADCB60733
18	20.2	67.3	86592	AB222285
19	20.2	67.3	86592	AAI57236
20	20.2	67.3	86592	AAI60240

C	21	20	66.7	1571	2	AAZ06546	AAZ06546 Lazy 1a1
C	22	20	66.7	28198	10	ADG37080	Adg37080 Mouse pla
C	23	19.8	66.0	1473	2	AAZ28295	Aaz28295 Rat neuro
C	24	19.8	66.0	2852	4	ABLI0572	Abli0572 Drosophi1
C	25	19.8	66.0	12260	4	ABLO8874	Ablo8874 Drosophi1
C	26	19.6	65.3	311	3	AAOC0837	Aac0837 Human sec
C	27	19.6	65.3	373	3	AAOC0838	Aac0838 Human sec
C	28	19.6	65.3	384	8	ABX39244	Abx39244 Bovine ES
C	29	19.6	65.3	501	3	AAOC3846	Aac03846 Human sec
C	30	19.6	65.3	516	13	ADOS2128	Ados2128 Novel can
C	31	19.6	65.3	762	8	ACA27881	Aca27881 Prokaryot
C	32	19.6	65.3	1024	12	ADU40088	AdU40088 Plant cdn
C	33	19.6	65.3	1475	6	ABLI61912	Abli61912 Colon ade
C	34	19.6	65.3	1550	13	ACN38710	Acn38710 Tumour-as
C	35	19.6	65.3	1623	10	ADSO8797	Adso8797 Novel DNA
C	36	19.6	65.3	1717	5	ABV20232	Abv20232 Human pro
C	37	19.6	65.3	1717	5	ABV26061	Abv26061 Human pro
C	38	19.6	65.3	1891	10	ADBS3729	Adbs3729 Human pro
C	39	19.6	65.3	2076	6	ABK35195	Abk35195 Human cdn
C	40	19.6	65.3	4258	4	AAK68397	Aak68397 Human imm
C	41	19.6	65.3	203070	11	ACN44012	Acn44012 Mouse gen
C	42	19.4	64.7	26329	4	AAK42041	Aak42041 Mouse s
C	43	19.4	64.7	236246	12	ADQ97590	Adq97590 Mouse can
C	44	19.2	64.0	401	4	AAK93385	Aak93385 Human neu
C	45	19.2	64.0	401	4	AAK96878	Aak96878 Human neu

## ALIGNMENTS

RESULT 1	ADCB7532	standard; DNA; 1273 BP.
ID	ADCB7532	
XX	ADCB7532	
AC	ADCB7532	
DT	01-JAN-2004	(first entry)
XX		
DE	Human GPCR gene SEQ ID NO:1985.	
XX		
KW	des; gene; human; GPCR;	
KM	guanosine triphosphate-binding protein coupled receptor; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1270724-A2.	
XX		
PD	02-JAN-2003.	
XX		
PF	18-JUN-2002; 2002EP-00013517.	
XX		
PR	18-JUN-2001; 2001JP-00246789.	
XX		
PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.	
XX	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.	
XX		
PI	Suwa M, Asai K, Akiyama Y, Aburatani H;	
XX		
DR	WPI; 2003-315783/31.	
XX	P-PSDB; ADCB7533.	
PT	New polynucleotide, useful for preparing a composition for treating a	
XX	patient in need of increased or suppressed activity or expression of the	
PT	guanosine triphosphate-binding protein coupled receptor.	
XX		
PS	Claim 1; SEQ ID NO 1985; 28pp; English.	
XX		
CC	The invention relates to a novel polynucleotide encoding a guanosine	
CC	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of	
CC	the invention may have a use in gene therapy. The polynucleotide and	
CC	polypeptide are useful for preparing a composition for treating a patient	
CC	in need of increased or suppressed activity or expression of the	
CC	guanosine triphosphate-binding protein coupled receptor. The	

CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the  
CC invention.  
XX  
SQ Sequence 1273 BP; 444 A; 84 C; 126 G; 518 T; 0 U; 101 Other;  
Query Match 70.7%; Score 21.2; DB 10; Length 1273;  
Best Local Similarity 82.1%; Pred. No. 75;  
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TAAATAGCTCTGTTATATGCTATATG 28  
DB 855 TATATACTCTGTATATATATATATG 882  
RESULT 2  
AAH54021  
ID AAH54021 standard; DNA; 2982 BP.  
XX  
AC AAH54021;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3385.  
XX  
KM Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;  
XX endocarditis; ds.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN WO200134809-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US030782.  
XX  
PR 09-NOV-1999; 99US-0164258P.  
XX  
XX (GLAX ) GLAXO GROUP LTD.  
PA  
XX kimmerly wj;  
PI  
XX WPI; 2001-316495/33.  
DR  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis.  
XX  
PS Claim 8; Page 938-939; 2188pp; English.  
XX  
CC AAH5304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)  
CC and (II) can have antibacterial activity and therefore can be used in  
CC vaccination. The nucleic acids (I) may be used to produce the S.  
CC epidermidis polypeptides (II) via the production of vectors containing  
CC them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to AAH5098  
CC represent oligonucleotide sequences and primers which are used in the  
CC exemplification of the present invention. N.B. The present invention  
CC specifically claims all the polynucleotide sequences given in the  
CC sequence listing of the present specification, however the sequence  
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
CC in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present  
CC for SEQ ID NO:4455 to 4464  
XX  
SQ Sequence 2982 BP; 753 A; 592 C; 434 G; 1203 T; 0 U; 0 Other;  
Query Match 70.7%; Score 21.2; DB 4; Length 2982;  
Best Local Similarity 82.1%; Pred. No. 82;

Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 3 AATATGCTCTGTTATATGCTATATGCT 30  
DB 42 AATGACTCTGTATATATGCTTTATGCT 69  
RESULT 3  
AAH54660  
ID AAH54660 standard; DNA; 3226 BP.  
XX  
AC AAH54660;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4024.  
XX  
KM Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;  
XX endocarditis; ds.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN WO200134809-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 09-NOV-2000; 2000WO-US030782.  
XX  
PR 09-NOV-1999; 99US-0164258P.  
XX  
XX (GLAX ) GLAXO GROUP LTD.  
PA  
XX kimmerly wj;  
PI  
XX WPI; 2001-316495/33.  
DR  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis.  
XX  
PS Claim 8; Page 1702-1703; 2188pp; English.  
XX  
CC AAH5304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)  
CC and (II) can have antibacterial activity and therefore can be used in  
CC vaccination. The nucleic acids (I) may be used to produce the S.  
CC epidermidis polypeptides (II) via the production of vectors containing  
CC them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to AAH5098  
CC represent oligonucleotide sequences and primers which are used in the  
CC exemplification of the present invention. N.B. The present invention  
CC specifically claims all the polynucleotide sequences given in the  
CC sequence listing of the present specification, however the sequence  
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
CC in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present  
CC for SEQ ID NO:4455 to 4464  
XX  
SQ Sequence 3226 BP; 727 A; 643 C; 518 G; 1338 T; 0 U; 0 Other;  
Query Match 70.7%; Score 21.2; DB 4; Length 3226;  
Best Local Similarity 82.1%; Pred. No. 82;  
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 3 AATATGCTCTGTTATATGCTATATGCT 30  
DB 3154 AATGACTCTGTATATATGCTTTATGCT 3181



DE	Full length human cDNA useful for treating neurological disease Seq 547.	XX
XX	gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;	KW
KW	osteoporosis; neurological disease; Alzheimer's disease;	KW
KW	Parkinson's disease; dementia; short memory; cancer;	KW
KW	sense or motor function; emotional reaction; fear response; panic;	KW
KW	osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;	KW
XX	tranquilliser.	XX
OS	Homo sapiens.	OS
XX		XX
PN	EP1447413-A2.	PN
XX		XX
PD	18-AUG-2004.	PD
XX		XX
PF	12-FEB-2004; 2004EP-00003145.	PF
XX		XX
PR	14-FEB-2003; 2003JP-00102207.	PR
XX		XX
PR	09-MAY-2003; 2003JP-00131452.	PR
XX		XX
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	PA
PI		PI
PI	Isegaai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;	PI
PI	Wakamatsu A, Ishii S, Nagai K, Irie R;	PI
XX		XX
DR	WPI; 2004-583265/57.	DR
DR	P-PSDB; ADR08997.	DR
XX		XX
PT	New 1995 cDNA, useful for treating osteoporosis, neurological diseases,	PT
XX	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.	XX
PS	Claim 1; SEQ ID NO 547; 2686bp; English.	PS
XX		XX
CC	This invention relates to novel, isolated full length human cDNA	CC
CC	molecules and the encoded proteins thereof. Specifically, it refers to	CC
CC	cDNA clones obtained by an oligo-capping method, where none of these	CC
CC	clones are identical to any known human mRNAs. The present invention	CC
CC	describes an immunoassay to identify agonists and antagonists, as well as	CC
CC	antibodies, antisense molecules and siRNAs that can all be used to bind	CC
CC	to and modulate expression of the cDNA molecules. As such, these	CC
CC	molecules are useful for diagnostic markers or therapeutic targets for	CC
CC	the various diseases or morbid states. In particular, they are useful in	CC
CC	gene therapy for treating osteoporosis, neurological disease, Alzheimer's	CC
CC	disease, Parkinson's disease, dementia, short memory and various cancers,	CC
CC	as well as for maintaining equilibrium of sense or motor function, and	CC
CC	for treating emotional reaction, fear response and panic. Accordingly,	CC
CC	they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,	CC
CC	cyostatic and tranquilliser activities. This polynucleotide is a full	CC
CC	length human cDNA sequence of the invention. NOTE: This sequence is not	CC
CC	given in the sequence listing of the specification but can be obtained on	CC
CC	CD-ROM from the European Patent Office, Vienna Sub-office.	CC
XX		XX
SQ	Sequence 1781 BP; 443 A; 400 C; 417 G; 521 T; 0 U; 0 Other;	SQ
XX		XX
Query Match	69.3%; Score 20.8; DB 13; Length 1781;	
Best Local Similarity	84.6%; Pred. No. 1,1e+02;	
Matches	22; Conservative 1; Mismatches 3; Indels 0; Gaps 0	
OY	3 AATATGCTCTGTRTATGCTATATG 28	
DB	557 AATTGTTCTGTGTATATTCATATG 582	

ID		AB06646 standard; cDNA; 6291 BP.
XX		
AC		ABL06646;
XX		
DT		26-MAR-2002 (first entry)
XX		
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 14420.	
XX		
KM	Drosophila; developmental biology; cell signalling; insecticide;	
KW	pharmaceutical; gene; ss.	
XX		
OS	Drosophila melanogaster.	
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	23-MAR-2001; 2001WO-US009231.	
PP		
PR	23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.	
XX		
PA	(PEKE ) PE CORP NY.	
PI	Venter JC, Adams M, Li PWD, Myers EW;  WI; 2001-656860/75. DR P-PADB; ABB62543.	
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.	
PT		
PS	Claim 1; SEQ ID NO 14420; 21pp + Sequence Listing; English.	
XX		
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABI16176-ABI10511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB52072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC		
CC		
SQ	Sequence 6291 BP; 1880 A; 1261 C; 1237 G; 1913 T; 0 U; 0 Other;	
Query Match	68.7%; Score 20.6; DB 4; Length 6291;	
Best Local Similarity	79.3%; Pred. No. 1.5e+02;	
Matches   23; Conservative     1; Mismatches       5; Indels      0; Gaps          0;		
OY	2 AAATAGTCTGTRATATGCTATATGCT 30	
	:	
Db	2621 ATATTGGCTTAATAAATGAATTGTACT 2593	
RESULT 6		
ABA16118/C		
ID	ABA16118 standard; DNA; 32216 BP.	
XX		
AC	ABA16118;	
XX		
DT	23-JAN-2002 (first entry)	
XX		
DE	Human nervous system related polynucleotide SEQ ID NO 8449.	
XX		
KM	Human; nootropic; neuroprotective; cyostatic; dermatological; virucide;	
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;	
KW	antiparkinsonian; antiskinking; antianaemic; anticarditic; cancer;	
KW	antihaematic; hepatoprotect; cerebroprotective; antiinflammotory;	
KW	antiallergic; antidabetic; anticancer; anticonvulsant; antifungal;	
KW	antipsychotic; cardiant; immune disorder; cardiovascular disorder;	

KM neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
XX Homo sapiens.  
XX WO200159063-A2.  
XX 16-AUG-2001.  
PF 17-JAN-2001; 2001WO-US001334.  
XX  
PR 31-JAN-2000; 2000US-0179066P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198122P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 11-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0217456P.  
PR 26-JUL-2000; 2000US-0218230P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
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PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225276P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 18-AUG-2000; 2000US-0225759P.  
PR 22-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 23-AUG-2000; 2000US-0227182P.  
PR 30-AUG-2000; 2000US-0227009P.  
PR 01-SEP-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 05-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 12-SEP-2000; 2000US-0232081P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
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PR 21-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
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PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246174P.  
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PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 17-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249266P.  
PR 01-DEC-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 08-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
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PR 08-DEC-2000; 2000US-0251989P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

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XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides.
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX Disclosure; SEQ ID NO 8449; 1701bp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABA1678-ABA18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 32216 BP; 7528 A; 8136 C; 7649 G; 8903 T; 0 U; 0 Other;
SQ
Query Match 68.7%; Score 20.6; DB 5; Length 32216;
Best Local Similarity 79.3%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 AAATATGCTCTGTTATATGCTATATGCT 30
Db 22719 AAATATTCACGTGCTGCTATATGCT 22691
RESULT 7
AAF58067/c
ID AAF58067 standard; DNA; 39198 BP.
XX
XX AAF58067;
XX
XX 26-APR-2001 (first entry)
XX
XX Human polyamine-modulated factor-1 PMF-1 gene.
XX
XX Human; polyamine-modulated factor-1; PMF-1; cancer; ds.
XX
XX Homo sapiens.
XX
XX WO200107610-A1.
XX
XX 01-FEB-2001.
XX
XX 21-JUL-2000; 2000WO-US019994.
XX
XX 23-JUL-1999; 99US-0145347P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Casero RA, Wang Y, Pegg AE;
XX
XX WPI; 2001-168553/17.
XX
XX P-PSDB; AAB68986.
XX
XX New nucleic acid encoding human polyamine-modulated factor-1 for
PT regulating a polyamine-modulated factor-1-responsive, polyamine-dependent
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PT gene in a cancerous cell.
XX
XX Claim 40; Fig 2; 61pp; English.
XX
XX The present invention provides the protein, coding and genomic sequences
CC of the human polyamine-modulated factor-1 protein (PMF-1). The sequences,
CC antibodies and analogues of the protein, are useful in the treatment
CC of cancer, via regulation of the spermidine/spermine N1-acetyltransferase
CC (SSAT) gene. The present sequence is the PMF-1 gene
XX
XX Sequence 39198 BP; 9083 A; 9915 C; 9191 G; 11002 T; 0 U; 7 Other;
SQ
Query Match 68.7%; Score 20.6; DB 5; Length 39198;
Best Local Similarity 79.3%; Pred. No. 1.8e+02;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 AAATATGCTCTGTTATATGCTATATGCT 30
Db 28830 AAATATTCACGTGCTGCTATATGCT 28802
RESULT 8
AAK81745/c
ID AAK81745 standard; DNA; 46553 BP.
XX
XX AAK81745;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36557.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
XX
XX 24-FEB-2000; 2000US-0184664P.
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XX 02-MAR-2000; 2000US-0186350P.
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XX 11-JUL-2000; 2000US-0217496P.
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XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0225267P.
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XX 14-AUG-2000; 2000US-0225268P.
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XX 14-AUG-2000; 2000US-0225270P.
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XX 14-AUG-2000; 2000US-0225447P.
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XX 14-AUG-2000; 2000US-0225758P.
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XX 14-AUG-2000; 2000US-0225759P.
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XX 18-AUG-2000; 2000US-0226279P.
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PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
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PR 21-SEP-2000; 2000US-0234223P.  
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PR 27-SEP-2000; 2000US-0235484P.  
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PR 08-NOV-2000; 2000US-0246609P.  
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PR 17-NOV-2000; 2000US-0249207P.  
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PR 17-NOV-2000; 2000US-0249244P.  
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PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 08-DEC-2000; 2000US-0251479P.  
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PR 08-DEC-2000; 2000US-0251862P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 05-JAN-2001; 2000US-0254097P.  
PR 05-JAN-2001; 2000US-0259678P.  
  
(HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483426/52.  
XX  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX  
XX Disclosure; SEQ ID NO 36557; 3071bp + Sequence Listing; English.  
XX  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
XX activity, and can be used in gene therapy and vaccine production. (I)  
XX proteins and polynucleotides may be used in the prevention, diagnosis and  
XX treatment of diseases associated with inappropriate (I) expression. For  
XX example, they may be used to treat disorders associated with decreased  
XX expression by rectifying mutations or deletions in a patient's genome  
XX that affect the activity of (I) by expressing inactive proteins or to  
XX supplement the patient's own production of (I). Additionally, (I)  
XX polynucleotides may be used to produce the secreted (I), by inserting the  
XX nucleic acids into a host cell and culturing the cell to express the  
XX protein. (I) proteins and polynucleotides may be used to prevent,  
XX diagnose and treat immune/hematopoietic-related diseases, especially  
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
XX to AAK87694 represent human immune/hematopoietic antigen genomic  
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
XX represent sequences used in the exemplification of the present invention  
XX  
XX  
SQ Sequence 46553 BP; 10776 A; 11618 C; 11092 G; 13067 T; 0 U; 0 Other;  
  
Query Match 68.7%; Score 20.6; DB 4; Length 46553;  
Best Local Similarity 79.3%; Pred. No. 1.9e+02;  
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2 AATATGCTGTRATATGCTATATGCT 30  
DB 37056 AATATTCAGTGTGCTATATGCT 37028

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RESULT 9
AK67926/c
ID AK67926 standard; DNA; 46553 BP.
XX
AC AK67926;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22738.
XX
KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KM cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
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PR 29-SEP-2000; 2000US-0236368P.
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PR 08-NOV-2000; 2000US-0246475P.
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PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249264P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
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CC The invention relates to a method of determining susceptibility of an  
CC individual to joint space narrowing and/or osteophyte development and/or  
CC joint pain comprising identifying whether the individual has at least one  
CC polymorphism in a polynucleotide encoding at least one of the protein  
CC listed in the specification. The methods, composition and agent are  
CC useful for modulating the susceptibility of an individual to joint space  
CC narrowing and/or osteophyte development and/or joint pain that is  
CC associated with a disease, preferably osteoarthritis. The cell line and  
CC the non-human animal are useful for screening for an agent for diagnosing  
CC an individual having susceptibility to joint space narrowing and/or  
CC osteophyte development and/or joint pain. This sequence corresponds to  
CC the polynucleotide encoding a protein listed in the specification. (Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences).

XX  
SQ Sequence 167932 BP; 42550 A; 42808 C; 42441 G; 40130 T; 0 U; 3 Other;

Query Match 68.7%; Score 20.6; DB 10; Length 167932;  
Best Local Similarity 79.3%; Pred. No. 2.1e+02;  
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 2 AATATGCTGCTGTATATGCTATATGCT 30  
Db 47208 AATATTCACGTGCTGCTATATGCT 47236

RESULT 12  
ABLO5214  
ID ABL05214 standard; cDNA; 4141 BP.  
XX  
AC ABL05214;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10124.  
DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KM pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009221.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
XX  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
DR P-PSDB; ABB61111.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
CC  
XX  
PS Claim 1; SEQ ID NO 10124; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signaling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
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SQ Sequence 4164 BP; 982 A; 1023 C; 1048 G; 1088 T; 0 U; 0 Other;

Query Match 68.0%; Score 20.4; DB 4; Length 4164;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 ATATGCTGCTGTATATGCTATAT 27  
Db 252 ATATGCTCTATATATGCTGAT 275

RESULT 13  
ABLO5338  
ID ABL05338 standard; cDNA; 4164 BP.  
XX  
AC ABL05338;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10496.  
DE  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KM pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
XX  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
DR P-PSDB; ABB61235.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
CC  
XX  
PS Claim 1; SEQ ID NO 10496; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 4164 BP; 947 A; 1030 C; 1101 G; 1086 T; 0 U; 0 Other;

Query Match 68.0%; Score 20.4; DB 4; Length 4164;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 ATATGCTGCTGTATATGCTATAT 27  
Db 1990 ATATGCTCTATATATGCTGAT 2013

RESULT 14





Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TAAATATGCTCTGTGTATATGCTATAT 27

Db 896 TCAATATATCTCTGTGTATATGCTACTAT 922

Search completed: February 14, 2005, 22:43:20  
Job time : 433 secs

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OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 22:17:03 ; Search time 487 Seconds  
(without alignments)  
363.478 Million cell updates/sec

Title: SEQ1-191TO220  
Perfect score: 30  
Sequence: 1 taaatagctctgtrtatatgcctatgc 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA: \*  
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2: /cgn2\_6/prodata/2/pubpna/PCr\_NEW\_PUB.seq: \*  
3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq: \*  
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7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq: \*  
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10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq: \*  
12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq: \*  
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16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq: \*  
17: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq: \*  
18: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq: \*  
19: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq: \*  
20: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq: \*  
21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq: \*  
22: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.2	74.0	78953	17	US-10-085-117-31
2	21.2	70.7	381	18	US-10-437-963-3640
3	21.2	70.7	1273	15	US-10-017-161-2339
4	21.2	70.7	1273	17	US-10-292-798-1985
5	20.8	69.3	42079	19	US-10-741-600-17906
C 6	20.8	69.3	260549	19	US-10-741-600-17906
7	20.6	68.7	1174	13	US-10-027-632-254267
8	20.6	68.7	1174	17	US-10-027-632-254267
9	20.6	67.3	59001	17	US-10-173-718-13
C 10	20.2	67.3	359	18	US-10-674-124A-12383
11	20.2	67.3	507	13	US-10-027-632-246790

12	20.2	67.3	507	13	US-10-027-632-246791	Sequence 246791,
13	20.2	67.3	507	17	US-10-027-632-246790	Sequence 246790,
14	20.2	67.3	507	17	US-10-027-632-246791	Sequence 246791,
15	20.2	67.3	2967	15	US-10-128-714-428	Sequence 428, App
16	20.2	67.3	3423	15	US-10-128-714-5428	Sequence 5428, App
17	20.2	67.3	15548	15	US-10-311-455-2128	Sequence 2128, App
C 18	20.2	67.3	86592	16	US-10-211-160-1	Sequence 1, Appl1
C 19	20.2	67.3	86592	16	US-10-051-681A-1	Sequence 1, Appl1
C 20	20.2	67.3	118356	18	US-10-741-600-17643	Sequence 17643, A
C 21	20.2	67.3	338287	19	US-10-741-601-5719	Sequence 5719, Ap
C 22	20.2	67.3	338287	19	US-10-741-600-17839	Sequence 17839, A
C 23	20	66.7	438	13	US-10-027-632-184011	Sequence 184011,
C 24	20	66.7	438	13	US-10-027-632-184011	Sequence 184011,
C 25	20	66.7	612	18	US-10-425-115-54267	Sequence 54267, A
C 26	20	66.7	45606	17	US-10-085-117-253	Sequence 253, App
C 27	19.8	66.0	1473	10	US-09-244-805-42	Sequence 42, Appl
C 28	19.8	66.0	1473	10	US-09-245-277-42	Sequence 42, Appl
C 29	19.8	66.0	1473	18	US-10-792-481-42	Sequence 42, Appl
C 30	19.6	65.3	201	19	US-10-741-600-72448	Sequence 72448, A
C 31	19.6	65.3	264	17	US-10-242-535A-49282	Sequence 49282, A
C 32	19.6	65.3	264	17	US-10-085-783A-49282	Sequence 49282, A
C 33	19.6	65.3	377	17	US-10-242-535A-57512	Sequence 57512, A
C 34	19.6	65.3	377	17	US-10-085-783A-57512	Sequence 57512, A
C 35	19.6	65.3	384	9	US-09-960-352-4409	Sequence 4409, Ap
C 36	19.6	65.3	410	17	US-10-242-535A-23682	Sequence 23682, A
C 37	19.6	65.3	410	17	US-10-085-783A-23682	Sequence 23682, A
C 38	19.6	65.3	448	18	US-10-674-124A-14835	Sequence 14835, A
C 39	19.6	65.3	762	17	US-10-282-122A-15751	Sequence 15751, A
C 40	19.6	65.3	1024	17	US-10-260-238-1088	Sequence 1088, App
C 41	19.6	65.3	1475	18	US-09-873-367C-249	Sequence 249, App
C 42	19.6	65.3	1717	18	US-10-357-930-20223	Sequence 20223, A
C 43	19.6	65.3	1717	18	US-10-357-930-20223	Sequence 20223, A
C 44	19.6	65.3	1891	16	US-10-252-157-75	Sequence 26050, A
C 45	19.6	65.3	2076	9	US-09-822-849A-333	Sequence 76, Appl

#### ALIGNMENTS

RESULT 1  
US-10-085-117-31/c  
Sequence 31, Application US/10085117  
Publication No. US20030232334A1  
GENERAL INFORMATION:  
APPLICANT: Morris, David W.  
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
FILE REFERENCE: 529452000121  
CURRENT APPLICATION NUMBER: US/10/085, 117  
CURRENT FILING DATE: 2002-02-27  
PRIOR APPLICATION NUMBER: US 09/798, 586  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 361  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 78953  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: variation  
LOCATION: (1)...(78953)  
OTHER INFORMATION: n = any nucleotide  
US-10-085-117-31

Query Match 74.0%; Score 22.2; DB 17; Length 78953;  
Best Local Similarity 82.8%; Pred. No. 1.1e+02;  
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TAAATAGCTCTGTRTATATGCTATATGC 29  
Db 12194 TCATTATACCTCTGTATATGCTATATGC 12166

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RESULT 2
US-10-437-963-3640
; Sequence 3640, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3640
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10597C.1
US-10-437-963-3640

Query Match      70.7%; Score 21.2; DB 18; Length 381;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 AATATGCTCTGTATATGCTATATGCT 30
DB      343 AATATCTCTATATATCTGCTATATGCT 370

RESULT 3
US-10-017-161-2339
; Sequence 2339, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2339
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1073)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (445)..(544)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (597)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-2339
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Query Match      70.7%; Score 21.2; DB 15; Length 1273;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTATATGCTATATG 28
DB      855 TATATATCTCTGTATATATATATATG 882

RESULT 4
US-10-292-798-1985
; Sequence 1985, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1985
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1073)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (445)..(544)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (597)..(597)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1985

Query Match      70.7%; Score 21.2; DB 17; Length 1273;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTATATGCTATATG 28
DB      855 TATATATCTCTGTATATATATATATG 882

RESULT 5
US-10-741-600-17906
; Sequence 17906, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17906
; LENGTH: 42079
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```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17906

Query Match
Best Local Similarity 69.3%; Score 20.8; DB 19; Length 42079;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAATATGCTCTGTTATATGCTATAT 27
Db 35433 ATATATGCTATATATATATGCTATAT 35458

RESULT 6
US-10-741-600-17723/C
; Sequence 17723, Application US/10741600
; Publication No. US2005026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MUCOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17723
; LENGTH: 260549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17723

Query Match
Best Local Similarity 69.3%; Score 20.8; DB 19; Length 260549;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAATATGCTCTGTTATATGCTATAT 27
Db 141470 ATATATGCTATATATATATGCTATAT 141445

RESULT 7
US-10-027-632-254267
; Sequence 254267, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254267
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254267
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Query Match
Best Local Similarity 68.7%; Score 20.6; DB 13; Length 1174;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TAAATATGCTCTGTTATATGCTATATGC 29
Db 953 TAAAGATCCTCTRTCTACATGCTGATGC 981

RESULT 8
US-10-027-632-254267
; Sequence 254267, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254267
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254267

Query Match
Best Local Similarity 79.3%; Score 20.6; DB 17; Length 1174;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TAAATATGCTCTGTTATATGCTATATGC 29
Db 953 TAAAGATCCTCTRTCTACATGCTGATGC 981

RESULT 9
US-10-173-718-13
; Sequence 13, Application US/10173718
; Publication No. US20030232437A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF VEGF-C EXPRESSION
; FILE REFERENCE: PLS-0036
; CURRENT APPLICATION NUMBER: US/10/173,718
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO 13
; LENGTH: 59001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10057-10156
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
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NAME/KEY: misc.feature  
LOCATION: 53857-53956  
OTHER INFORMATION: n = A,T,C or G  
US-10-173-718-13

Query Match 68.7%; Score 20.6; DB 17; Length 59001;  
Best Local Similarity 85.2%; Pred. No. 4.4e+02;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAATATGCTCTGTATATGCTATATG 28  
Db 33098 AAATATGCTCTGTATATGCTATATG 33124

RESULT 10

US-10-674-124A-12383/c  
Sequence 12383, Application US/10674124A  
Publication No. US20040197797A1  
GENERAL INFORMATION:

APPLICANT: INOKO, Hidetoshi  
APPLICANT: TAMURA, Gen  
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
FILE REFERENCE: ORIN-003CIP  
CURRENT APPLICATION NUMBER: US/10/674,124A

PRIOR FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 10/257,511  
PRIOR FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: PCT/JP00/07621  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: JP2000-112699  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: JP2002-327516  
PRIOR FILING DATE: 2002-09-28  
PRIOR APPLICATION NUMBER: JP2002-383869  
PRIOR FILING DATE: 2002-12-09  
NUMBER OF SEQ ID NOS: 27110  
SEQ ID NO 12383

LENGTH: 359

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: AC004957.1\_93436

FEATURE:

OTHER INFORMATION: Located on chromosome 7

FEATURE:

OTHER INFORMATION: Distance between a terminus base of telomere on

OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base

FEATURE: sequence: 86314220

OTHER INFORMATION:

OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of

OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and

OTHER INFORMATION: 5'-terminus of this base sequence: 6547

US-10-674-124A-12383

Query Match 67.3%; Score 20.2; DB 18; Length 359;  
Best Local Similarity 81.5%; Pred. No. 2.9e+02;

Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATG 27  
Db 137 TATATATGCTGTATATGCTATATG 111

RESULT 11

US-10-027-632-246790

Sequence 246790, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 246790  
LENGTH: 507  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-246790

Query Match 67.3%; Score 20.2; DB 13; Length 507;  
Best Local Similarity 75.9%; Pred. No. 3e+02;  
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATGC 29  
Db 256 TAAATATTTTGAATTTCTGCTATATGC 284

RESULT 12

US-10-027-632-246791

Sequence 246791, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 246791

LENGTH: 507

TYPE: DNA

ORGANISM: Human

US-10-027-632-246791

Query Match 67.3%; Score 20.2; DB 13; Length 507;  
Best Local Similarity 75.9%; Pred. No. 3e+02;  
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATGC 29  
Db 256 TAAATATTTTGAATTTCTGCTATATGC 284

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RESULT 13
US-10-027-632-246790
; Sequence 246790, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246790
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-246790

Query Match      67.3%; Score 20.2; DB 17; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRATATGCTATATGC 29
Db      256 TAAATATMTTGTGAATTTCTGCTATATGC 284

RESULT 14
US-10-027-632-246791
; Sequence 246791, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246791
; LENGTH: 507
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-246791

Query Match      67.3%; Score 20.2; DB 17; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRATATGCTATATGC 29
Db      256 TAAATATMTTGTGAATTTCTGCTATATGC 284

RESULT 15
US-10-128-714-428
; Sequence 428, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskinin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 2967
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-428

Query Match      67.3%; Score 20.2; DB 15; Length 2967;
Best Local Similarity 81.5%; Pred. No. 4e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRATATGCTATAT 27
Db      441 TCAATATACTCTGTGATATGCACTAT 467
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Search completed: February 14, 2005, 22:52:57  
Job time : 489 secs

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